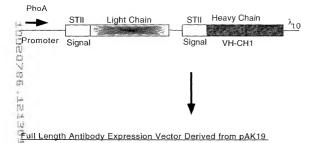
Fab Expression Vector pAK19



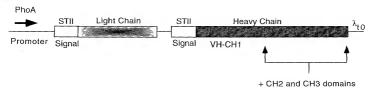


Figure 1

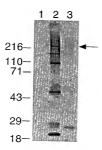


Figure 2

Polycistronic Constructs

AP promot	er STII	light chain	STII	heavy chain	λto trans. term.
	TIR		TIR		
	1		1	paTF20	
	3		1	paTF30	
	1		3	paTF40	
11	3		3	paTF90	
many of the state	7		3	paTF110	
(1) (1)	3		7	paTF100	
hair hair	7		7	paTF120	

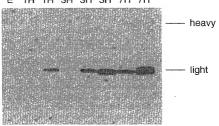
Figure 3.

4A

4B

polycistronic reduced

o 1L 3L 1L 3L 7L 3L 7L 2 1H 1H 3H 3H 3H 7H 7H



polycistronic non-reduced

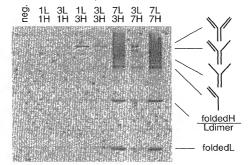
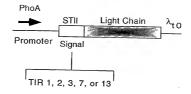


Figure 4

Light Chain Constructions



Heavy Chain Constructions

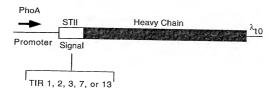


Figure 5

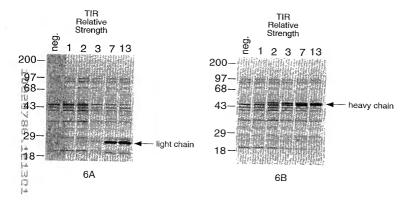


Figure 6

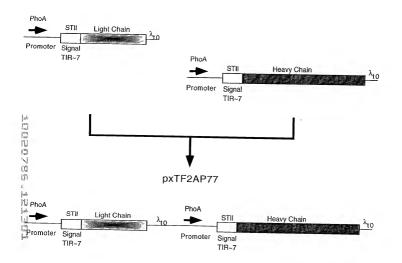


Figure 7

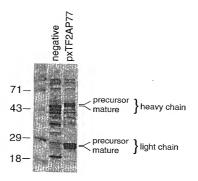


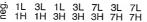
Figure 8

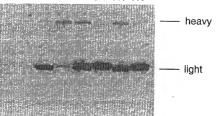
Separate Cistron Constructs

AP promote	r STII	light chain	λ to trans. term.	AP promoter	STII	heavy chain	λ to trans. term.
[2] L							
	TIR			7	ΓIR		
	1				1	paTF50	
i. Joseph	3				1	paTF70	
NJ 	1			;	3	paTF60	
T T T	3			;	3	paTF80	
ţ-m	7			;	3	paTF130	
	3			7	7	paTF140	
	7			7	7	pxTF2AP77	

Figure 9

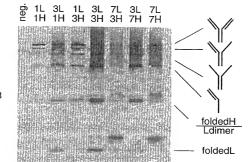
separate cistrons reduced





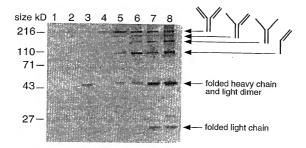
10A

separate cistrons non-reduced



10B

Figure 10



- 1) negative control
- 2) TIR 1-light, TIR 1-heavy, polycistronic
- 3) TIR 3-light, TIR 1-heavy, polycistronic
- 4) TIR 1-light, TIR 3-heavy, polycistronic
- 5) TIR 1-light, TIR 1-heavy, separate cistrons
- 6) TIR 1-light, TIR 3-heavy, separate cistrons
- 7) TIR 3-light, TIR 1-heavy, separate cistrons
- 8) TIR 3-light, TIR 3-heavy, separate cistrons

Figure 11

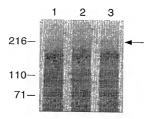


Figure 12

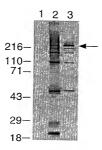


Figure 13

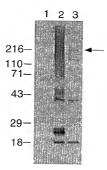


Figure 14

Figure 15

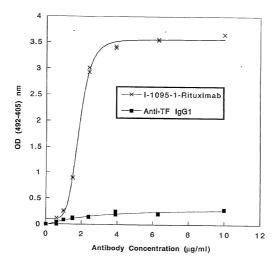


Figure 16

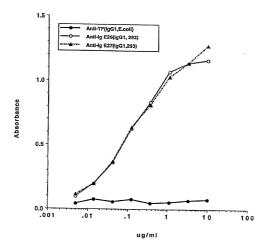


Figure 17

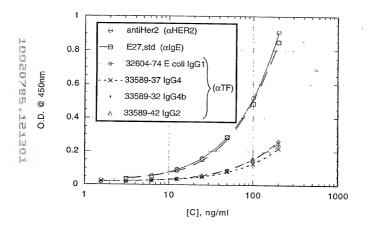


Figure 18

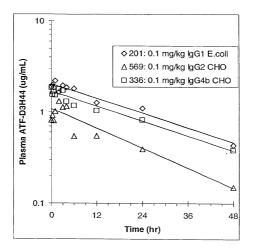


Figure 19

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- ООСЛИТАТОО СОСЛАЛАТСА СОМСЛЕСКЕ ТТЕМТЕВЛЕ ЛЕТАЛОВЛЕДО ОВСОСТОТА. СВЛОТВАЛОС ССЕЛТОСТОЛ СМІТЕСТВЕ СВСЕМИТЕСТВ ОСОТРАТАСС ССЕПТІЛЬСТ СОПТОТОССЕ ЛАСТАЛСТВО ТСЕЛГЕТССЕ СОВСЬЯСАТЕ СПОСМІТТСЕ СВСЕЛЬСВОГЕ СПЛАБАЛТВ СТВЕТИЛОСЕ
- 1501 JACTOSCTIT GITITIATIT ITTRAGGIAI IIGIBACHAG TACSCHAGIT CACGHARAA GGGINICTAG AATLAIGAAG AAGANATGG CAITICTICT ATCHGCBAR CARAATARA AANTHCHA AAATTACHA AIGCGTTCHA GTGCATTTIT CCCATRGATC TTAATACTIC TTCTTATAGC GTRAAGAAGA 1401 AGCIGCIBGG GBATIACGIA AAGAAGIINI IGAAGGAIGG ICGICAGINA AAAGIIAAIC ITIICAACAG CIGICAIAAA GIIGICAGG GGGAACTIA ICGACGACGC GCTAATGCAT TICTICAATA ACTTCGTAGG AGCAGTCATI TITCAATTAG AAAAGTIGIC GACAGTATIT CAACAGTSCC GGCTCTGAAT

^STII Signal Sequence TIR-1

- 1601 IGCATCTANG TICGTITITI CTATIGCTAC AAAOGOGTAC GCTGAGGTIC AGCTGGTGGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG CTCACTCCGT GAGTGAGGCA ACCTAGATAC AAGGAAAAA GATAACGATG TITGGSCATG CGACTCCAAG TGGACCACCT CAGACGGCCA CCGGACCACG TCGGTCCCCC G L V A E V Q L V E S G G G Anti-Tissue Factor Heavy Chain N A Y T V I 5 4 4
- 1701 TISTECTOTS CASCITCISS CITCAATAIT AASSAGTACT ACAISCACIS SGICCOICAS SCCCCOSGAA AGGGCIGGA AIGGGIIGGA IIGAATIGAI AACAGACAC GTCGAAGACC GAAGTTATAA TTCCTCATGA TGTACGTGAC CCAGGCAGTC GGGGGCCCAT TCCCGGACCT TACCCAACCT AACTAACTAG
 - 1801 CAGAGGAAGG CAACACGATC TATGACCCGA AGTTCCAGGA CCGTGCCACT ATAAGGGCTG ACAATTCCAA AAACACAGCA TACCTGCAGA TGAACAGCCT S > 3 GLB A P G K 0 2 2 MHM KEYY × A S G 43 L S C A
 - ATGGACGTCT ACTTGTCGGA Y LOM TITGIGICGE NTA GGCACGGTGA TATTCGCGAC TGTTAAGGTT I S A D N S K RAT TCAAGGTCCT Y D P K P Q D GICTOSTICC GIIGIGCIAG AIACHGGGCI E E
 - CTSTUNCEGC AGATAATAAC ACGAGCTCTG TGCCGGCGAA TGAAGCTGAT GACCCCAGTT CCTTGGGACC AGTGGCAGAG GAGCGGGAGG .901 GCGTGCTGAG GACACTGCCG TCTATTATTG TGCTCGAGAC ACGGCCGCTT ACTTCGACTA CTGGGGTCAA GGAACCCTGG TCACCGTCTC > > O T I 0 9 F D Y TAAY ARD XX DIAV CGCACGACTC 110 R A E
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- SCRATGOR CAGCACTTG AGTOCGGGG ACTGGTGGC GCACGTGTGG AAGGGCGAC AGGATGTCAG GAGTCCTGAG ATGAGGGAGT CGTCGCACA CTCAGGACTC TACTCCCTCA GCAGCGTGGI Y S L S SGL 2101 CGGTGACGGT GTCGTGGAAC TCAGGCGCC TGACCAGCGG CGTGCACACC TTCCCGGCTG TCCTACAGTC r o N M dd dd A H T S G SGAL N N N 177
- 2201 GACTETECC TCTAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTGGACA AGAAGTTGA GCCCAAATCT TICCACCIGI ICITICAACI CGGGIITIAGA K V D K CIGGALGIAG ACGITGCACT TAGIGITCOG GICGITGIGG S ж CNVN TXI CTGACACGGG AGATOGTOGA ACCCGTGGGT G T D S S S
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STCCT CACCGTCCT CAGGA GTGGCAGGA	CTCCAAAGCC AAAGGGCAGC C GAGGTTTCGG TTTCCCGTCG G S K A K G Q P	STICT ATCCCAGCGA	CTTCTTCCT CTACAGO BAAGAAGCA GATGTCG F F L Y S	AGAAG AGCCTCTCCC CTTC TCGGAGAGGG K S L S L	GACA GCTTATC	COATC CTCGGCA GATAG GAGCCGTA F Sequence	AGTC ACTATGG	
TACCGTGTGG TCAGCGTCCT ATGGCACACC AGTCGCAGGA Y R V V S V L	MACCAT CTCCAL TTGGTA GAGGT: T I S K	CTGCCTGGTC AAAGGCTTCT SACGGACCAG TTTCCGAAGA C L V K G F Y	TCCGACGGCT CCTTCT AGGCTGCCGA GGAAGA S D G S F F	CCACTA CACGCAC GGTGAT GTGCGTC H Y T Q	TAACTC ATGTTI ATTGAG TACAAA	TGCGCT CATCG1 ACGCGA GTAGCA Stance Coding	SACAGO ATOGOO CIGTOG TAGOSG	
CAACAGCACG TACC GTIGTCGTGC ATGG N S T Y R	GCCCCCATCG AGAMACCAT CGGGGGTAGC TCTTTTGGTA A P I B K T I	TCAGCCTGAC CTGO AGTCGGACTG GACG	CGTCCTGGAC TCCG GCACGACCTG AGGC V L D S D	GAGGCTCTGC ACAAC CTCCGAGACG TGTTC E A L H N	SCGITITITA INGI:	MIGMANICIA ACANIGGGT CATCGTONIC CTCS PACTINGAT IGTINGGGA GINGCNGING SAGO Start Tet Resistance Coding Sequence	ATATCGICCA TICCK	
SG AGGAGCAGTA SC TCCTCGTCAT E E Q Y	A AGCCCTCCCA T TOGGGAGGGT	C AAGAACCAGG 3 TTCTTGGTCC I K N Q V	A CCAGGCCTCC OF GGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CGTGATGCAT S GCACTACGTA V M H I	AACGCCCCCC	A GGCACCGTGT 2	CTCTTGCGGG A	
AAGCCGCGG	TCTCCAACAA AGAGGTTGTT SNK	TCTCTACTGC	AACTACAAGA TTGATGTTCT N Y K T	AGAGTACGAG	TAACGCTCGC	AACGCAGTCA	ACTGCCGGGC TGACGGCCCG	
ACCCAAGACA ACCCTTCTGT	AAGTGCAAGG TTCACGTTCC	GTAGGGCCCT S R E	GCCGGAGAAC CGGCCTCTTG P E N	GGGAACCTCT CCCTTGCAGA G N V F	CIAGAGICCC	TTAAATTGCT AATTTAACGA	TTATGCCGGT AATACGGCCA	
310	343	2701	2801	2901	3001	3101	3201	

AAATACAGAC ATGAAAAATC TCATTSCTGA GTTGTTATTT AAGCTTGCCC AAAAGAAGA AGAGTCGA TTTATGTCTG TACTTTTAG AGTAAGGACT CAACAATAAA TTGGAACGGG TTTTTCTTCT TCTCAGCTT
C TCATIGCTGA GTRGTTATTT AAGCE
TCATTGCTGA GTTG
TCATTG
AAATACAGAC AIGAAAAATC TTTATGTCTG TACTTTTTAG
AAATACAGAC TTTATGTCTG
TTGGATAAGG
TCTCCATACT
1 GAATTCAACT CTTAAGTTGA

- 101 GALCINITAD GOCAGINA ACCTITAGAS ATTATOGROA, CICOLATOCT FICICLATATA GOCOLALATO ACCACAGO, GITCATTOLT CAGGRAGO CONTINUTA CAGGRAGO, CITURACACO GOTICATOR CAGGRAGO, GOCOTITADO ROCOTITADO ROC CCCBATGCCA GCATTCCTGA CGACGATACG GAGCTGCTGC GOGATTACCT AAAGAAGTTA ITGAAGCATC CTCGTCAGYA CTOGACGACG CGCTAATGCA TITCTICAAT AACTICGIAG GAGCAGICAT CCCGCGACAT GCTCCATTIC GGGCTACGGT CGTAAGGACT GCTGCTATGC GGGCGCTGTA CGAGGTAAAG 201
- 101 ARARGITAR CITITOACA GURICATA AGTURCAGO GCCAGAGOT ARAGOGOT TUTUTURI TITUAZOR HURIRACIA GREGOLAGI ITITOATIA GAAAGITGI GACAGTATI TOACAGOGO COGCUCAGA ARCAGOGA ACADAATIA ABARTACAF DAROGUTGA.
- AGTSCATTIT TCCCATAGAT CTTAATACTT CTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA AGATAACGAT GTTYGCGCAT GCGACTATAG TIGCATCIAI GIICGIIIII ICIAIIGCIA CAAAGGGGIA CGCIGAIAIC Anti-VEGF Light chain^ SIATNAY A A A S M 401 TCACGTAAAA AGGGTATCTA GAATTATGAA GAAGAATATC GCATTTCTTC AFLL *STII Signal TIR ~1 M
- 881 CAGTIGACCC AGTCCCCGAG CTCCCTGTCC GCCTCTGGG GCGATAGGGT CACCATCACC ISCAGGGCAA GTCAGGATAT IAGCAACTAT TTAAACTGGT STCAACTOGG TCAGGGGCTC GAGGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTGG ACGTCGCGTT CAGTCCTATA ATCGTTGATA AATTTGACCA I Q O CSAS LIL DRV SLSASVG
- - S 9 9 9 SR d A D SLHS F T APKVLIY P G 9
- 701 GANTTCACT CTOACURDA GEAGTURCA, GCUGARAGAC TUCGORACTI ATTACTORTA ACAGRINAGE ACCORDICOT GAAGOTITGA ACAGGUING CCTARACTOR GACTOGRAF COTOAGACOT COGNICTICTA RAGOSTIGAA TAATGACAGT TOTCATATAG TGGGAGGGA. 801 ARGSTGGAGA TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC T P G M d A I Q Y S N C FATY D E E S L O 93 D F T
 - TUCCACTET AGTITGETTO ACACCBAGGI GGINGACAGA AGIAGAGGG CGGINGACIA CICGICAACI IINGACETIG ACGAAGACAA CACACGGACG GTCACAGAGC AGGACAGCAA CAGTGTCTCG TCCTGTCGTT A S V 901 TGARTAACIT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGGTAACIC CCAGGAGAGT COGGAGGITA GCCCATTGAG GGTCCTCTCA E 0 S O E BOLK G N S ALQS D S ACTIVITICAA GAIAGGGICT CTCCGGTITC AIGTCACCIT CCACCIAING d d I N Q A P S V F N K BAKV VAA X X 126 K V E I
- 001 GONCHOCHEC THENGESTEN GENGEREET GREGETGRGS AANGERGAET AEGRGAANEN CHAAGTETAE GESTGEGAAG TERCECATER GGGESTGAGE CCTGTCGTGG ATGTCGGAGT CGTCGTGGGGACT CTCGTCTCA TGTCGTCTTAGT GTTTCAGATG CGGACCCTTC AGTGGGTAGT D S T Y S L S S T L T L S K A D Y R K H K V Y A C E V T H Q
- 1101 TOGCCOTCA CAAAGAGTT CAACAGGGA GAGTUTAAF TAAATCCTCT AGGCCGAGG CATCGTGGG AGTCGAFAC CGGGGGATT AGGCCTAAG AGGGGGAT GTTCTCGAA GTTGTCCCCT CTCACAATTA ATTAGGAGA TGCGGCCTGC GTAGCACGC TGGAGCCATG GGCCCTAGA TCGGAATTGC E C O S N S 226 S P V T

1201 G	rcggttgc Agccaacg(C GCCGGGCGT.	CHOSTINCC GOOGGOOTT TITALTUST GOOGGOOGE ATCTCBATG AACTGTOGTOG GCAGGTAGA GCTTGGAGA TAATGGTOG TGCAATGCTT GAGCDAOGG GGGCCCGGAA AAAATAACA CGGCTGOOGG TAGAGCTTAC TTGACACAGG CGTCCATCTT GGAAACGTCT AATAGAGGTG ACGTTACGAA	CGGCTGCGC	ATCTCGAATG TAGAGCTTAC	AACTGTGTGC TTGACACACG	GCAGGTAGAA CGTCCATCTT	GCTTTGGAGA	TTATCGTCAC	TGCAATGCTT
1301 00	CCCAATATGG	G GCGTTTTACT	CCCAATATGG CCCAAAATGA CCAACAGGGG TTGATTGATC GCGTTATACT GGTTGTGGCC AACTAACTAG	CCAACAGCGG TYGATTGATC AGGTAGAGGG GROCTGTAC GAGGTAAAGC CCGATGCCAG GGTTGTGGCC AACTAACTAG TCCATCTCCC CCGGGACATG CTCCATTTGG GGCTACGGTC	AGGTAGAGGG TCCATCTCCC	GGCGCTGTAC	GAGGTAAAGC	CCGATGCCAG	CCGATGCCAG CATTCCTGAC GGCTACGGTC GTAAGGACTG	GACGATACGG
1401 AG	SCTOCTGC	GCTAATGCGTZ	AGCICCIGOS COATTACGIA AAGAACITAT TGAAGCATCC TOSTCAGTAA TOSACGACGO GCTAAIGCAT TICTICAATA ACTTOGIAGG AGCAGTOATI	TGAAGCATCC	TCGTCAGTAA		AAAGTTAATC TTTTCAACAG TTTCAATTAG AAAAGTTGTC	CTGTCATAAA GACAGTATTT	CTGTCATAAA GTTGTCACGG GACAGTATTT CAACAGTGCC	CCGAGACTTA
1501 TA AT	TAGECGCTTT ATCAGCGAAA	F GTTTTTATTA A CAAAATAAA	tronggraa caaratra aattrontr atcaggraa caaratrar aattrontr	TIGEAACTAG	TACGCAAGTT ATGCGTTCAA	TTGTAACTAG TACGCAAGTI CACGTAAAAA AACATIGATC ATGCSTTCAA GTGCATTTTT	GGGTATCTAG	AATTATGAAG TTAATACTTC M K ^ STII	AATTATGAAG AAGAATATCG TTAATACTTC TTCTTATAGC M K K N I A ^STII SİGNƏN TIR-1	CATTICITOT GTANAGAAGA F L L
1601 TGC ACC 10 A	TGCATCTATG ACGTAGATAC A S M	TTCGTTTTT BAGCAAAAA FVFS	TTOSTITUTI CRATHSCENA AMAGGOSTAG CGTBAGGTTC AGCTGGTGGA GTCTGGGGGT AGCTAAAA GATAAGGATT TTGGGGAYG CGTGCCAGA GTGCGCCTC CAACGGCA F V V B S I A T N A Y A B V O L V B S O G $^{\prime\prime}$ Anti-VSGF Heavy Chain	AAACGCGTAC TTTGCGCATG N A Y	GCTGAGGTTC CGACTCCAAG A B V Q Anti-VE	AAACGCGTAC GCTGAGGTTC AGCTGGTGGA GCAG. TTTGGGCATC CAAG TCCAACAACT AG. N A Y A B V Q L V B S ^Anti-V88F Heavy Chain	GTCTGGCGGT CAGACCGCCA S G G	GGCCTGGTGC CCGGACCACG G L V Q	GGCCTGGTGC AGCCAGGGGG CCGGACCACC TCGGTCCCCC G L V Q P G G	CTCACTCCGT GAGTGAGGCA S L R
1701 TT AA 43 L	TTGTCCTGTG AACAGGACAC L S C A	GAGCTTCTGG	CTACGACTIC GATGCTGAAG Y D F	ACGCACTACG TGCGTGATGC T H Y G	GTATGAACTG CATACTTGAC M N W	GGTCCGTCAG CCAGGCAGTC V R Q	GCCCCGGGTA CGGGGCCCAT A P G K	GENTGACTG GETCCGTCAG GCCCGGGTA AGGCCCTGGA CATACTTGAC CCAGGCAGTC CGGGGCCCTT TCCCGGACCT M N W V R Q A P G K G L E	ATGGGTTGGA TACCCAACCT W V G	TGGATTAACA ACCTAATIGT W I N T
20 75	1801 CCTATACCGG GGATATGGCC 77 Y T G		TGAACCGACC TATGCTGCGG ALTTCAAACG ACTTCGCTGG ATACGACGCC TAAAGTTTGC E P T Y A A D F K R	ATTTCAAACG TAAAGTTTGC F K R	TCGTTTCACT AGCAAAGTGA R F T		TTTTCTTTAG ACACCTCCAA AAAAGAAATC TGTGGAGGTF F S L D T S K	TITICITING ACACCICCAA AAGCACAGCA AAAAGAAATC ICHGGAGGTI ITCGTCTCGT F S L D T S K S I A	TACCTGCAGA ATGGACGTCT Y L Q M	TGAACAGCCT ACTTGTCGGA N S L
1901 GCC CGC 110 R	GCGCGCTGAG CGCGCGACTC R A B	GACACTGCCG CTGTGACGCC	TCTATTACTG AGATAATGAC Y Y C	TGCAAAGTAC ACGTTTCATG A K Y	CCGTACTATT GGCATGATAA P Y Y Y	ACCGCACGAG TGCCGTGCTC G T S	CCACTGGTAT GGTGACCATA H N Y	TTCGACGTCT AAGCTGCAGA F D V W	GGGGTCAAGG CCCCAGTTCC G Q G	AACCCTGGTC TTGGGACCAG T L V
001 AC TG(2001 ACCGTCTCCT TGGCAGAGGA 143 T V S S	OGGCCTCCAC GCCGCAGGTG A S T	CAAGGGCCCA GTTCCCGGGT K G P	TCGGTCTTCC AGCCAGAAGG S V P P	CCCTGGCACC GGGACCGTGG L A P	CTCCTCCAAG GAGGAGGTTC S S K	AGCACCTCTG TCGTGGAGAC S T S G	GGGGCACAGC CCCCGTGTCG G T A	GGCCTGGGC CCGGGACCCG A L G	TGCCTGGTCA ACGGACCAGT C L V K
101 AGC TCC	2101 AGGACTACTT TCCTGATGAA 177 D Y F	CCCCGAACCG GGGGCTTGGC P E P	GTGACGGTGT CACTGCCACA V T V S	CGTGGAACTC GCACCTTGAG W N S	AGGOGCOCTG TCCGCGGGAC G A L	ACCAGOGGGG TGGTCGCCGC	TOCACACCTT CCCGGCTGTC ACGIGTGGAA GGGCCGACAG H T F P A V	TGCACACCTT CCCGGCTGTC CTACAGTCCT ACCTVTGGAA GGGCCGACAG GATGTCAGGA H T F P A V L Q S S		CAGGACTCTA GTCCTGAGAT G L Y
2201 CTC GAC 210 S	CTCCCTCAGC GAGGGAGTOG S L S	AGCGTGGTGA TCGCACCACT S V V T	CTGTGCCCTC GACACGGGAG V P S	TAGCAGCTTG ATCGTCGAAC S S L	GCACCCAGA CCGIGGGICT G I Q I	CCTACATORG GGATGTAGAC Y I C	CAACGIGAAT GITGCACTIA N V N	CACAAGCCCA GTGTTCGGGT H K P S	GCAACACCAA CGTTGTGGTT N T K	GGTGGACAAG CCACCTGTTC V D K
301 AA/ TTT 243 K	2301 AAAGTTGAGC TTTCAACTCG 243 K V E P		TGACAAACT ACTGTTTTGA D K T	CACACATGCC GTGTGTACGG H T C P	CACCGTGCCC GTGGCACGGG	AGCACCTGAA TCGTGGACTT A P E	CTCCTSGGGG GAGGACCCCC L L G G	CTCCTGGGGG GACCGTCAGT CTTCCTCTTC GAGGACCCC CTGGCAGTCA GAAGGAGAAG L L G G P S V F L F		CCCCCAAAC GGGGTTTTG P P K P
401 CCP GGT 277 K	MAGGACAC STICCIGIG K D I	CCTCATGATC GGAGTACTAG L M I	2401 COMGGACIC CETGATGATE TOCKGGACCC CTGAGGATCAC ATGOGGGGGG GTGGACCTGA GCCACGAGA CCTGAGGAC AGGACCACA GACCACGAGGACCAG GACCACGAGGACCAG GACCACGAGGACCAG GACCACGAGGACCAG GACCACGAGGACCAG GACCACGAGGACAGAGAGACAGA AGGACACAGAGAGAG	GACTCCAGTG	TACGCACCAC	GTGGACGTGA	GCCACGAAGA CGGTGCTTCT	CCTGAGGTC	AAGTICAACT	GGTACGTGGA

2501 CERCITEGAS GROUNTAING CHARARDAA GROEGOGINGA ARAGOARGTA COTTOTOGICA ARAGOARGTOS COUTOTOGICA CHAGARTOS CONTROLAS GROCGOCCOTO CONTROLAS GROCARGOARGA GROCARGOARGA GROCARGOARGA GROCARGA ARAGOARGA GROCARGA GROCARGA GROCARGA GROCARGA ARAGOARGA GROCARGA GR	1601 CTGANTGGO, AGANGTACA, REGALAGANG CCCCCCCCC CCCCCNTGAG ANAICANTCT CCCAAGACCAA AGGRCJACCC CGAGAACCAC MANTICACT PICTOANTC AACOTTOCA AGANTSTOTT COGAGAACCA TITGATAA AGANTGGAT TACCATAGA TACCATAGA TACATAGA TACATA	1701 AGDITANAC COTACCCO, TOCOMBAG MARKACAGIT ARCTINICA CONTOUTO'S AGAITICHY COCACGORACA TOCACGORACA TOCACGORACA TOCACGORACA GAAGAGGG AGAICACHA BA TA TOCACACACT TOCACACACA TA	NOT GROBANACA ANTOGENAC ORGANICAN CRICANSACA CONSTITUTO TOUTOSACTIC CONCESSENCE TECTIVETED ACADEMACT CONCESSENCE CONCESSENCE OFFICE ANTOGENACIAN ANTOGEN ANTOGEN ANTOGEN ANTOGEN ANTOGEN ANTOGEN ANTOGEN OF S. P. P. P. P. P. D. B. D. G. B. P. F. E. Y. S. R. E. T. V. V. R. F. P. P. V. E. D. S. D. G. S. P. F. E. Y. S. R. E. T. V. V. V. S. N. G. C. P. S. R. E. F. E. P. V. E. D. S. D. G. S. P. F. E. Y. S. R. E. T. V.	1901 ANGHOLAGA GEORGAGO GAMGATUTE TUATGUTGO TRATECHTA GOCTOCOCO ALCOATRA GEORGAGAGA CETTUCCOS TUCUCARRA TUTUCTUCA CANTOSTOC CITUCADAAA ALFANAGAGA CANTOSTATO COGRAGORA TATATATA OSTUTUTUS GORANAGAGA CANTOSTA CANTOSTA ALFA K S R W G O G W W F S C S V W H E A H M H A R T T G K S L S C S V	3901 ARTAGONIO CARCESCUT MAGNOCCH, ACCUTOSTI COCOCCOSCO CITITIANI CITIACICA TITIACICA TITICACACA TACCAGARA PAGNOCCA CARCAGARA CALTEGRA CAACTUTO ANTAGOTA EXTURANTA CAACTUTO ANTAGOTA EXTURANTA TITICACACA CACACACA A CACACACACA CACACACA CACACACA CACACACA CACACACA CACACACA CACACACA CACACACA CACACACA CACACACACA CACACACA CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA CA	1101 TECHTALT TREACHET AANTOCHA COOKTOMB OACOTOTH CAAATCHAC ANTOCHCA TOTOCHCAC CORROCKE EACOTOMAC ACCONTOA ATMOTICA TITAACAATT GEREARTO GINGORDA CITTAACAATT OACOTOMA COORTIOCHCAC TOTOCHCACA ATMOTICA AT	1201 CUSTAGENT AGGETIGENT ANDOCOGRAG TOCCOGRACOT CYTGOGGAT ANDOCOCAT, COACAGOOT COCCAGURO, PANDAGOSTO, TOCCHAGAGT ANDOCOCATA ANDOCOCATA AGGETICAGA, ANDOCOCATA AGGETICAGA, ANDOCOCATA ANDOCOCATA AGGETICAGA, ANDOCOCATA ANDOCOCATA AGGETICAGA.	
A CCGTCCTGCA F GGCAGGACGT	AGGGCAGC	r cccagogaca A gggrcgcrgr P S D I	r ACAGCAAGCT A TGTCGTTCGA	CCTCTCCC	TTATCATO	T CGGCACCC A GCCGTGGC	TATGGCG1	
AGCGTCCTCA TCGCAGGAGT S V L T	CCAAAGCCAA GGTTTCGGTT K A K	AGGCTICTAI TCCGAAGAIA G F Y	TTCTTCCTCT AAGAAGGAGA F F L Y	CGCAGAAGAG GCGTCTTCTC Q K S	GTTTGACAGC	TCGTCATCCT AGCAGTAGGA ding Sequer	CCCCAGTCAC	
CCGTGTGGTC GGCACACCAG R V V	AAAACCATCT TTTTGGTAGA K T I S	GCCTGGTCAA CGGACCAGIT L V K	CGACGGCTCC GCTGCCGAGG D G S	AACCACTACA TTGGTGATGT N H Y T	GTTAACTCAT CAATTGAGTA	AATGCGCTCA TTACGCGAGT Sistance Co	CCGACAGCAT	
ACAGCACGIA TGTCGTGCAT S T Y	CCCCATOGAG GGGGTAGCTC P I B	AGCCTGACCT GCCTGGTCAA TCGGACTGGA CGGACCAGTI S L T C L V K	TGCTGGACTC ACGACCTGAG L D S	GGCTCTGCAC CCGAGACGTG A L H	GITITITATI CAAAAATAA	T GARATCTAG ANIGGETCA TOGICATOR O A CTITAGATIG TIACGOGNGI AGCAGINGGA G Start Tet Resistance Coding Sequence	ATCGTCCATT	
GAGCAGTACA CTCGTCATGT E Q Y N	TCCAACAAAG CCCTCCCAGC AGGTTGTTC GGGAGGGTCG S N K A L P A	GAACCAGGTC CTTGGTCCAG N Q V	ACGCCTCCCG TGCCGAGGGC Z	TGATGCATGA ACTACGTACT M H E	0000000000	CACCGTGTAT GTGGCACATA	CTTGCGGGAT	
GCCGCGGGAG CGGCGCCCTC PRB	TCCAACAAAG AGGTTGTTTC S N K A	AGATGACCAA TCTACTGGTT M T K	CTACAAGACC GATGTTCTGG Y K T	TCATGCTCOG AGTACGAGGC S C S V	ACGCTCGGTT	CGCAGTCAGG	TGCCGGGCCT	
CCRAGACAAA GGTTCTGTTT K T K	GTGCAAGGTC CACGTTCCAG C K V	TCCCGGGAAG AGGGCCCTTC S R B E	CGGAGAACAA GCCTCTTGTT E N N	GAACGICTIC CITGCAGAAG N V F	AGAGTCCCTA	AAATTGCTAA TTTAACGATT	ATGCCGGTAC TACGGCCATG	
GTGCATAATG CACGTATTAC V H N A	AGGAGTACAA TCCTCATGTT E Y K	CCTGCCCCCA GGACGGGGGT L P P	AATGGGCAGC TTACCCGTCG N G Q P	GGCAGCAGGG CCGTCGTCCC Q Q G	CGACGGCCCT	TATCACAGIT	AGGCTTGGTT TCCGAACCAA	
CGGCGTGGAG GCCGCACCTC G V E	CTGAATGGCA GACTTACCGT L N G K	AGGIGIACAC TCCACAIGIG V Y I	GTGGGAGAGC CACCCTCTGG W E S	901 AAGAGCAGGT TICTCGTCCA 443 K S R W	AATAAGCATG TTATTCGTAC 0	TGCGGTAGTT	CTGTAGGCAT	
310	343	377	2801	2901	3001	3101	3201	3301

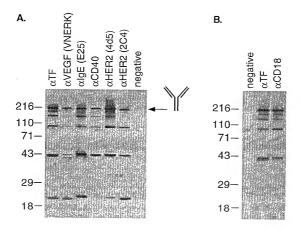


Figure 22